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Freyssinet, Georges
Perez, Pascal

<120> METHOD FOR OBTAINING PLANT VARIETIES

<130> A33153-PCT-USA 072667.0128

<140> US 09/529,239
<141> 2000-10-27

<150> PCT/EP98/06977
<151> 1998-10-09

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| gatataagtg | gtggttgtgg | tggtaagaa | ggtttggtt | cacagagtaa | tttcttggtt | 720 |
| tgtgttgtgg | atgagagagt | taagtcggag | acattaggct | gtggtattga | aatgagttt | 780 |
| gatgttagag | tcggtgtgt | tggcgttcaa | atttcgacag | gtgaagttgt | ttatgaagag | 840 |
| ttcaatgata | atttcatgag | aagtggatta | gaggctgtga | ttttgagctt | gtcaccagct | 900 |
| gagctgtgc | ttggccagcc | tcttcacaaa | caaactgaga | agtttttgggt | ggcacatgct | 960 |
| ggacacctac | caaacgttcg | agtggAACGT | gcctcaactgg | attgtttcag | caatggtaat | 1020 |
| gcagtagatg | aggtaatttc | attatgtgaa | aaaatcagcg | caggtaactt | agaagatgat | 1080 |
| aaagaaatga | agctggaggc | tgctgaaaaaa | ggaatgtctt | gcttgacagt | tcataacaatt | 1140 |
| atgaacatgc | cacatctgac | tgttcaagcc | ctgcgcctaa | cgtttgcca | tctcaaacag | 1200 |
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<212> DNA
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| tgaaaggatc | ctttaccaag | gggcctcatt | tcgcttttgc | tcaagtaaca | cagagatgac | 120 |
| tctctcagcc | aataactctgc | aacagtggaa | ggtttgaaa | aataattcag | atggatcgga | 180 |
| atctggctcc | ttattccata | atatgaatca | cacacttaca | gtatatggtt | ccaggcttct | 240 |
| tagacactgg | gtgactcattc | ctctatgcga | tagaaatttg | atatctgctc | ggcttgatgc | 300 |
| tgtttcttag | atttctgctt | gcatgggatc | tcatagttct | tcccagctca | gcagtgagtt | 360 |
| ggttgaagaa | ggttctgaga | gagcaattgt | atcacctgag | ttttatctcg | tgctctcctc | 420 |
| agtcttgaca | gctatgtcta | gatcatctga | tattcaacgt | ggaataacaa | aatctttca | 480 |
| tcggactgct | aaagccacag | agttcattgc | agttatggaa | gctattttac | ttgcggggaa | 540 |

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| gcaaattcag | cggctggca | taaagcaaga | ctctgaaatg | aggagtatgc | aatctgcaac | 600 |
| tgtcgatct | actctttga | aaaaatttat | ttctgttatt | tcatcccctg | ttgtgttga | 660 |
| caatgccgga | aaacttctct | ctgccctaaa | taaggaagcg | gctgttcgaa | gtgacttgct | 720 |
| cgacatacta | atcaccccca | gcgaccaatt | tcctgagctt | gctgaagctc | gccaagcagt | 780 |
| tttagtcattc | agggaaaagc | tggattcctc | gatacgctca | tttcgcaaga | agctcgctat | 840 |
| tcgaaatttg | gaatttcttc | aagtgtcgaa | gatcacacat | ttgatagagc | tgcccggttga | 900 |
| ttccaaggctc | cctatgaatt | gggtgaaagt | aaatagcacc | aagaagacta | ttcgatatac | 960 |
| tccccccagaa | atagtagctg | gcttggatga | gctagctcta | gcaactgaac | atcttgcatt | 1020 |
| tgtgaaccga | gcttcgtggg | atagtttctt | caagagtttc | agtagatact | acacagattt | 1080 |
| taaggctgcc | gttcaagctc | ttgctgact | ggactgtttt | cactccctt | caactctatc | 1140 |
| tagaaacaag | aactatgtcc | gtcccgagtt | tgtggatgac | tgtgaaccag | ttgagataaa | 1200 |
| catacagtct | ggtcgtcattc | ctgtactgg | gactatatta | caagataact | tcgtccaaa | 1260 |
| tgacacaattt | ttgcatgcag | aagggaaata | ttgccaaattt | atcaccggac | ctaacatggg | 1320 |
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| ctttgtacca | gcgtcattcg | ccaagctgca | cgtgcttgc | ggtgtttca | ctcgatggg | 1440 |
| tgcttcagac | agtatccagc | atggcagaag | taccttctt | gaagaattaa | tgaaacgtc | 1500 |
| acacataatc | agaacactgtt | cttctcggtt | gcttggatata | tttagatgagc | ttggaaagagg | 1560 |
| cactagcaca | cacgacgggt | tagccattgc | ctatgcaaca | ttacagcattc | tccttagcaga | 1620 |
| aaagagatgt | ttgggttctt | ttgtcacgca | ttaccctgaa | atagctgaga | tcagtaacgg | 1680 |
| attcccaagg | tctgttggg | cataccatgt | ctcgatctt | acattgcaga | aggataaaagg | 1740 |
| cagttatgt | catgtatgt | tgacctacct | atataagctt | gtgcgtggtc | tttgccggcag | 1800 |
| gagcttttgt | tttaaggttg | ctcagcttgc | ccagataacct | ccatcatgtt | tacgtcgagc | 1860 |
| catttcaatg | gctgcaaaat | tggaaagctga | ggtacgtgca | agagagagaa | atacacgcat | 1920 |
| gggagaacca | gaaggacatg | aagaaccgag | aggcgccagaa | gaatcttattt | cggctctagg | 1980 |
| tgacttggtt | gcagacctga | aatttgctct | ctctgaagag | gacccttgga | aagcattcga | 2040 |
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 <211> 3522
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<400> 18

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Met Gly Lys Gln Lys Gln Gln Thr Ile Ser Arg Phe Phe Ala Pro Lys
  1           5           10          15

ccc aaa tcc ccg act cac gaa ccg aat ccg gta gcc gaa tca tca aca 195
Pro Lys Ser Pro Thr His Glu Pro Asn Pro Val Ala Glu Ser Ser Thr
  20          25          30

ccg cca ccg aag ata tcc gcc act gta tcc ttc tct cct tcc aag cgt 243
Pro Pro Pro Lys Ile Ser Ala Thr Val Ser Phe Ser Pro Ser Lys Arg
  35          40          45

aag ctt ctc tcc gac cac ctc gcc gcc tca ccc aaa aag cct aaa 291
Lys Leu Leu Ser Asp His Leu Ala Ala Ser Pro Lys Lys Pro Lys
  50          55          60

ctt tct cct cac act caa aac cca gta ccc gat ccc aat tta cac caa 339
Leu Ser Pro His Thr Gln Asn Pro Val Pro Asp Pro Asn Leu His Gln
  65          70          75          80

aga ttt ctc cag aga ttt ctg gaa ccc tcg ccg gag gaa tat gtt ccc 387
Arg Phe Leu Gln Arg Phe Leu Glu Pro Ser Pro Glu Glu Tyr Val Pro
  85          90          95

gaa acg tca tca tcg agg aaa tac aca cca ttg gaa cag caa gtg gtg 435
Glu Thr Ser Ser Arg Lys Tyr Thr Pro Leu Glu Gln Gln Val Val
  100         105         110

gag cta aag agc aag tac cca gat gtg gtt ttg atg gtg gaa gtt ggt 483
Glu Leu Lys Ser Lys Tyr Pro Asp Val Val Leu Met Val Glu Val Gly
  115         120         125

tac agg tac aga ttc ttc gga gaa gac gcg gag atc gca gca cgc gtg 531
Tyr Arg Tyr Arg Phe Phe Gly Glu Asp Ala Glu Ile Ala Ala Arg Val
  130         135         140

ttg ggt att tac gct cat atg gat cac aat ttc atg acg gcg agt gtg 579
Leu Gly Ile Tyr Ala His Met Asp His Asn Phe Met Thr Ala Ser Val
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cca aca ttt cga ttg aat ttc cat gtg aga aga ctg gtg aat gca gga 627

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Pro Thr Phe Arg Leu Asn Phe His Val Arg Arg Leu Val Asn Ala Gly
 165 170 175
 tac aag att ggt gta gtg aag cag act gaa act gca gcc att aag tcc 675
 Tyr Lys Ile Gly Val Val Lys Gln Thr Glu Thr Ala Ala Ile Lys Ser
 180 185 190
 cat ggt gca aac cgg acc ggc cct ttt ttc cgg gga ctg tcg gcg ttg 723
 His Gly Ala Asn Arg Thr Gly Pro Phe Phe Arg Gly Leu Ser Ala Leu
 195 200 205
 tat acc aaa gcc acg ctt gaa gcg gct gag gat ata agt ggt ggt tgt 771
 Tyr Thr Lys Ala Thr Leu Glu Ala Ala Glu Asp Ile Ser Gly Gly Cys
 210 215 220
 ggt ggt gaa gaa ggt ttt ggt tca cag agt aat ttc ttg gtt tgt gtt 819
 Gly Gly Glu Glu Gly Phe Gly Ser Gln Ser Asn Phe Leu Val Cys Val
 225 230 235 240
 gtg gat gag aga gtt aag tcg gag aca tta ggc tgt ggt att gaa atg 867
 Val Asp Glu Arg Val Lys Ser Glu Thr Leu Gly Cys Gly Ile Glu Met
 245 250 255
 agt ttt gat gtt aga gtc ggt gtt ggc gtt gaa att tcg aca ggt 915
 Ser Phe Asp Val Arg Val Gly Val Val Gly Val Glu Ile Ser Thr Gly
 260 265 270
 gaa gtt gtt tat gaa gag ttc aat gat aat ttc atg aga agt gga tta 963
 Glu Val Val Tyr Glu Glu Phe Asn Asp Asn Phe Met Arg Ser Gly Leu
 275 280 285
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 Glu Ala Val Ile Leu Ser Leu Ser Pro Ala Glu Leu Leu Leu Gly Gln
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 cct ctt tca caa caa act gag aag ttt ttg gtg gca cat gct gga cct 1059
 Pro Leu Ser Gln Gln Thr Glu Lys Phe Leu Val Ala Met Ala Gly Pro
 305 310 315 320
 acc tca aac gtt cga gtg gaa cgt gcc tca ctg gat tgt ttc agc aat 1107
 Thr Ser Asn Val Arg Val Glu Arg Ala Ser Leu Asp Cys Phe Ser Asn
 325 330 335
 ggt aat gca gta gat gag gtt att tca tta tgt gaa aaa atc agc gca 1155
 Gly Asn Ala Val Asp Glu Val Ile Ser Leu Cys Glu Lys Ile Ser Ala
 340 345 350
 ggt aac tta gaa gat gat aaa gaa atg aag ctg gag gct gct gaa aaa 1203
 Gly Asn Leu Glu Asp Asp Lys Glu Met Lys Leu Glu Ala Ala Glu Lys
 355 360 365
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 Gly Met Ser Cys Leu Thr Val His Thr Ile Met Asn Met Pro His Leu
 370 375 380
 act gtt caa gcc ctc gcc cta acg ttt tgc cat ctc aaa cag ttt gga 1299
 Thr Val Gln Ala Leu Ala Leu Thr Phe Cys His Leu Lys Gln Phe Gly

| 385 | 390 | 395 | 400 | |
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| ttt gaa agg atc ctt tac caa ggg gcc tca ttt cgc tct ttg tca agt Phe Glu Arg Ile Leu Tyr Gln Gly Ala Ser Phe Arg Ser Leu Ser Ser | | | | 1347 |
| 405 | 410 | | 415 | |
| aac aca gag atg act ctc tca gcc aat act ctg caa cag ttg gag gtt Asn Thr Glu Met Thr Leu Ser Ala Asn Thr Leu Gln Gln Leu Glu Val | | | | 1395 |
| 420 | 425 | | 430 | |
| gtg aaa aat aat tca gat gga tcg gaa tct ggc tcc tta ttc cat aat Val Lys Asn Asn Ser Asp Gly Ser Glu Ser Gly Ser Leu Phe His Asn | | | | 1443 |
| 435 | 440 | | 445 | |
| atg aat cac aca ctt aca gta tat gct tcc agg ctt ctt aga cac tgg Met Asn His Thr Leu Thr Val Tyr Gly Ser Arg Leu Leu Arg His Trp | | | | 1491 |
| 450 | 455 | | 460 | |
| gtg act cat cct cta tgc gat aga aat ttg ata tct gct cgg ctt gat Val Thr His Pro Leu Cys Asp Arg Asn Leu Ile Ser Ala Arg Leu Asp | | | | 1539 |
| 465 | 470 | | 475 | 480 |
| gct gtt tct gag att tct gct tgc atg gga tct cat agt tct tcc cag Ala Val Ser Glu Ile Ser Ala Cys Met Gly Ser His Ser Ser Gln | | | | 1587 |
| 485 | 490 | | 495 | |
| ctc agc agt gag ttg gtt gaa gaa ggt tct gag aga gca att gta tca Leu Ser Ser Glu Leu Val Glu Glu Gly Ser Glu Arg Ala Ile Val Ser | | | | 1635 |
| 500 | 505 | | 510 | |
| cct gag ttt tat ctc gtg ctc tcc tca gtc ttg aca gct atg tct aga Pro Glu Phe Tyr Leu Val Leu Ser Ser Val Leu Thr Ala Met Ser Arg | | | | 1683 |
| 515 | 520 | | 525 | |
| tca tct gat att caa cgt gga ata aca aga atc ttt cat cgg act gct Ser Ser Asp Ile Gln Arg Gly Ile Thr Arg Ile Phe His Arg Thr Ala | | | | 1731 |
| 530 | 535 | | 540 | |
| aaa gcc aca gag ttc att gca gtt atg gaa gct att tta ctt gcg ggg Lys Ala Thr Glu Phe Ile Ala Val Met Glu Ala Ile Leu Leu Ala Gly | | | | 1779 |
| 545 | 550 | | 555 | 560 |
| aag caa att cag cgg ctt ggc ata aag caa gac tct gaa atg agg agt Lys Gln Ile Gln Arg Leu Gly Ile Lys Gln Asp Ser Glu Met Arg Ser | | | | 1827 |
| 565 | 570 | | 575 | |
| atg caa tct gca act gtg cga tct act ctt ttg aga aaa ttg att tct Met Gln Ser Ala Thr Val Arg Ser Thr Leu Leu Arg Lys Leu Ile Ser | | | | 1875 |
| 580 | 585 | | 590 | |
| gtt att tca tcc cct gtt gtg gtt gac aat gcc gga aaa ctt ctc tct Val Ile Ser Ser Pro Val Val Asp Asn Ala Gly Lys Leu Leu Ser | | | | 1923 |
| 595 | 600 | | 605 | |
| gcc cta aat aag gaa gcg gct gtt cga ggt gac ttg ctc gac ata cta Ala Leu Asn Lys Glu Ala Ala Val Arg Gly Asp Leu Leu Asp Ile Leu | | | | 1971 |
| 610 | 615 | | 620 | |

| | | |
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| atc act tcc agc gac caa ttt cct gag ctt gct gaa gct cgc caa gca | | 2019 |
| Ile Thr Ser Ser Asp Gln Phe Pro Glu Leu Ala Glu Ala Arg Gln Ala | | |
| 625 | 630 | 635 |
| 640 | | |
| gtt tta gtc atc agg gaa aag ctg gat tcc tcg ata gct tca ttt cgc | | 2067 |
| Val Leu Val Ile Arg Glu Lys Leu Asp Ser Ser Ile Ala Ser Phe Arg | | |
| 645 | 650 | 655 |
| aag aag ctc gct att cga aat ttg gaa ttt ctt caa gtg tcg ggg atc | | 2115 |
| Lys Lys Leu Ala Ile Arg Asn Leu Glu Phe Leu Gln Val Ser Gly Ile | | |
| 660 | 665 | 670 |
| aca cat ttg ata gag ctg ccc gtt gat tcc aag gtc cct atg aat tgg | | 2163 |
| Thr His Leu Ile Glu Leu Pro Val Asp Ser Lys Val Pro His Asn Trp | | |
| 675 | 680 | 685 |
| gtg aaa gta aat agc acc aag aag act att cga tat cat ccc cca gaa | | 2211 |
| Val Lys Val Asn Ser Thr Lys Lys Thr Ile Arg Tyr His Pro Pro Glu | | |
| 690 | 695 | 700 |
| ata gta gct ggc ttg gat gag cta gct cta gca act gaa cat ctt gcc | | 2259 |
| Ile Val Ala Gly Leu Asp Glu Leu Ala Leu Ala Thr Glu His Leu Ala | | |
| 705 | 710 | 715 |
| 720 | | |
| att gtg aac cga gct tcg tgg gat agt ttc ctc aag agt ttc agt aga | | 2307 |
| Ile Val Asn Arg Ala Ser Trp Asp Ser Phe Leu Lys Ser Phe Ser Arg | | |
| 725 | 730 | 735 |
| tac tac aca gat ttt aag gct gcc gtt caa gct ctt gct gca ctg gac | | 2355 |
| Tyr Tyr Thr Asp Phe Lys Ala Ala Val Gln Ala Leu Ala Leu Asp | | |
| 740 | 745 | 750 |
| tgt ttg cac tcc ctt tca act cta tct aga aac aag aac tat gtc cgt | | 2403 |
| Cys Leu His Ser Leu Ser Thr Leu Ser Arg Asn Lys Asn Tyr Val Arg | | |
| 755 | 760 | 765 |
| ccc gag ttt gtg gat gac tgt gaa cca gtt gag ata aac ata cag tct | | 2451 |
| Pro Glu Phe Val Asp Asp Cys Glu Pro Val Glu Ile Asn Ile Gln Ser | | |
| 770 | 775 | 780 |
| ggt cgt cat cct gta ctg gag act ata tta caa gat aac ttc gtc cca | | 2499 |
| Gly Arg His Pro Val Leu Glu Thr Ile Leu Gln Asp Asn Phe Val Pro | | |
| 785 | 790 | 795 |
| 800 | | |
| aat gac aca att ttg cat gca gaa ggg gaa tat tgc caa att atc acc | | 2547 |
| Asn Asp Thr Ile Leu His Ala Glu Gly Glu Tyr Cys Gln Ile Ile Thr | | |
| 805 | 810 | 815 |
| gga cct aac atg gga gga aag agc tgc tat atc cgt caa gtt gct tta | | 2595 |
| Gly Pro Asn Met Gly Gly Lys Ser Cys Tyr Ile Arg Gln Val Ala Leu | | |
| 820 | 825 | 830 |
| att tcc ata atg gct cag ggt tcc ttt gta cca gcg tca ttc gcc | | 2643 |
| Ile Ser Ile Met Ala Gln Val Gly Ser Phe Val Pro Ala Ser Phe Ala | | |
| 835 | 840 | 845 |

aag ctg cac gtg ctt gat ggt gtt ttc act cggt atg ggt gct tca gac 2691
 Lys Leu His Val Leu Asp Gly Val Phe Thr Arg Met Gly Ala Ser Asp
 850 855 860

 agt atc cag cat ggc aga agt acc ttt cta gaa gaa tta agt gaa gcg 2739
 Ser Ile Gln His Gly Arg Ser Thr Phe Leu Glu Glu Leu Ser Glu Ala
 865 870 875 880

 tca cac ata atc aga acc tgt tct tct cgt tcg ctt ata tta gat 2787
 Ser His Ile Ile Arg Thr Cys Ser Ser Arg Ser Leu Val Ile Leu Asp
 885 890 895

 gag ctt gga aga ggc act agc aca cac gac ggt gta gcc att gcc tat 2835
 Glu Leu Gly Arg Gly Thr Ser Thr His Asp Gly Val Ala Ile Ala Tyr
 900 905 910

 gca aca tta cag cat ctc cta gca gaa aag aga tgt ttg gtt ctt ttt 2883
 Ala Thr Leu Gln His Leu Leu Ala Glu Lys Arg Cys Leu Val Leu Phe
 915 920 925

 gtc acg cat tac cct gaa ata gct gag atc agt aac gga ttc cca ggt 2931
 Val Thr His Tyr Pro Glu Ile Ala Glu Ile Ser Asn Gly Phe Pro Gly
 930 935 940

 tct gtt ggg aca tac cat gtc tcg tat ctg aca ttg cag aag gat aaa 2979
 Ser Val Gly Thr Tyr His Val Ser Tyr Leu Thr Leu Gln Lys Asp Lys
 945 950 955 960

 ggc agt tat gat cat gat gat gtg acc tac cta tat aag ctt gtg cgt 3027
 Gly Ser Tyr Asp His Asp Asp Val Thr Tyr Leu Tyr Lys Leu Val Arg
 965 970 975

 ggt ctt tgc agc agg agc ttt ggt ttt aag gtt gct cag ctt gcc cag 3075
 Gly Leu Cys Ser Arg Ser Phe Gly Phe Lys Val Ala Gln Leu Ala Gln
 980 985 990

 ata cct cca tca tgt ata cgt cga gcc att tca atg gct gca aaa ttg 3123
 Ile Pro Pro Ser Cys Ile Arg Arg Ala Ile Ser Met Ala Ala Lys Leu
 995 1000 1005

 gaa gct gag gta cgt gca aga gag aga aat aca cgc atg gga gaa cca 3171
 Glu Ala Glu Val Arg Ala Arg Glu Arg Asn Thr Arg Met Gly Glu Pro
 1010 1015 1020

 gaa gga cat gaa gaa ccg aga ggc gca gaa gaa tct att tcg gct cta 3219
 Glu Gly His Glu Glu Pro Arg Gly Ala Glu Ser Ile Ser Ala Leu
 1025 1030 1035 1040

 ggt gac ttg ttt gca gac ctg aaa ttt gct ctc tct gaa gag gac cct 3267
 Gly Asp Leu Phe Ala Asp Leu Lys Phe Ala Leu Ser Glu Glu Asp Pro
 1045 1050 1055

 tgg aaa gca ttc gag ttt tta aag cat gct tgg aag att gct ggc aaa 3315
 Trp Lys Ala Phe Glu Phe Leu Lys His Ala Trp Lys Ile Ala Gly Lys
 1060 1065 1070

 atc aga cta aaa cca act tgt tca ttt tgatttaatc ttaacattat 3362

Ile Arg Leu Lys Pro Thr Cys Ser Phe
1075 1080

agcaactgca aggtcttgat catctgttag ttgcgtacta acttatgtgt attagtataa 3422
caagaaaaaga gaatttagaga gatggattct aatccggtgt tgcaagtacat cttttctcca 3482
cccgcataaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3522

<210> 19
<211> 1081
<212> PRT
<213> Arabidopsis thaliana ecotype Columbia
<223> Polypeptide MSH3

<400> 19

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Pro Lys Ser Pro Thr His Glu Pro Asn Pro Val Ala Glu Ser Ser Thr
20 25 30

Pro Pro Pro Lys Ile Ser Ala Thr Val Ser Phe Ser Pro Ser Lys Arg
35 40 45

Lys Leu Leu Ser Asp His Leu Ala Ala Ala Ser Pro Lys Lys Pro Lys
50 55 60

Leu Ser Pro His Thr Gln Asn Pro Val Pro Asp Pro Asn Leu His Gln
65 70 75 80

Arg Phe Leu Gln Arg Phe Leu Glu Pro Ser Pro Glu Glu Tyr Val Pro
85 90 95

Glu Thr Ser Ser Arg Lys Tyr Thr Pro Leu Glu Gln Gln Val Val
100 105 110

Glu Leu Lys Ser Lys Tyr Pro Asp Val Val Leu Met Val Glu Val Gly
115 120 125

Tyr Arg Tyr Arg Phe Phe Gly Glu Asp Ala Glu Ile Ala Ala Arg Val
130 135 140

Leu Gly Ile Tyr Ala His Met Asp His Asn Phe Met Thr Ala Ser Val
145 150 155 160

Pro Thr Phe Arg Leu Asn Phe His Val Arg Arg Leu Val Asn Ala Gly
165 170 175

Tyr Lys Ile Gly Val Val Lys Gln Thr Glu Thr Ala Ala Ile Lys Ser
180 185 190

His Gly Ala Asn Arg Thr Gly Pro Phe Phe Arg Gly Leu Ser Ala Leu
195 200 205

Tyr Thr Lys Ala Thr Leu Glu Ala Ala Glu Asp Ile Ser Gly Gly Cys
210 215 220

Gly Gly Glu Glu Gly Phe Gly Ser Gln Ser Asn Phe Leu Val Cys Val
225 230 235 240

Val Asp Glu Arg Val Lys Ser Glu Thr Leu Gly Cys Gly Ile Glu Met
245 250 255

Ser Phe Asp Val Arg Val Gly Val Val Gly Val Glu Ile Ser Thr Gly
260 265 270

Glu Val Val Tyr Glu Glu Phe Asn Asp Asn Phe Met Arg Ser Gly Leu
275 280 285

Glu Ala Val Ile Leu Ser Leu Ser Pro Ala Glu Leu Leu Leu Gly Gln
290 295 300

Pro Leu Ser Gln Gln Thr Glu Lys Phe Leu Val Ala Met Ala Gly Pro
305 310 315 320

Thr Ser Asn Val Arg Val Glu Arg Ala Ser Leu Asp Cys Phe Ser Asn
325 330 335

Gly Asn Ala Val Asp Glu Val Ile Ser Leu Cys Glu Lys Ile Ser Ala
340 345 350

Gly Asn Leu Glu Asp Asp Lys Glu Met Lys Leu Glu Ala Ala Glu Lys
355 360 365

Gly Met Ser Cys Leu Thr Val His Thr Ile Met Asn Met Pro His Leu
370 375 380

Thr Val Gln Ala Leu Ala Leu Thr Phe Cys His Leu Lys Gln Phe Gly
385 390 395 400

Phe Glu Arg Ile Leu Tyr Gln Gly Ala Ser Phe Arg Ser Leu Ser Ser
405 410 415

Asn Thr Glu Met Thr Leu Ser Ala Asn Thr Leu Gln Gln Leu Glu Val
420 425 430

Val Lys Asn Asn Ser Asp Gly Ser Glu Ser Gly Ser Leu Phe His Asn
435 440 445

Met Asn His Thr Leu Thr Val Tyr Gly Ser Arg Leu Leu Arg His Trp
450 455 460

Val Thr His Pro Leu Cys Asp Arg Asn Leu Ile Ser Ala Arg Leu Asp
465 470 475 480

Ala Val Ser Glu Ile Ser Ala Cys Met Gly Ser His Ser Ser Ser Gln
485 490 495

Leu Ser Ser Glu Leu Val Glu Glu Gly Ser Glu Arg Ala Ile Val Ser
500 505 510

Pro Glu Phe Tyr Leu Val Leu Ser Ser Val Leu Thr Ala Met Ser Arg
515 520 525

Ser Ser Asp Ile Gln Arg Gly Ile Thr Arg Ile Phe His Arg Thr Ala
530 535 540

Lys Ala Thr Glu Phe Ile Ala Val Met Glu Ala Ile Leu Leu Ala Gly
545 550 555 560

Lys Gln Ile Gln Arg Leu Gly Ile Lys Gln Asp Ser Glu Met Arg Ser
565 570 575

Met Gln Ser Ala Thr Val Arg Ser Thr Leu Leu Arg Lys Leu Ile Ser
580 585 590

Val Ile Ser Ser Pro Val Val Asp Asn Ala Gly Lys Leu Leu Ser
595 600 605

Ala Leu Asn Lys Glu Ala Ala Val Arg Gly Asp Leu Leu Asp Ile Leu
610 615 620

Ile Thr Ser Ser Asp Gln Phe Pro Glu Leu Ala Glu Ala Arg Gln Ala
625 630 635 640

Val Leu Val Ile Arg Glu Lys Leu Asp Ser Ser Ile Ala Ser Phe Arg
645 650 655

Lys Lys Leu Ala Ile Arg Asn Leu Glu Phe Leu Gln Val Ser Gly Ile
660 665 670

Thr His Leu Ile Glu Leu Pro Val Asp Ser Lys Val Pro His Asn Trp
675 680 685

Val Lys Val Asn Ser Thr Lys Lys Thr Ile Arg Tyr His Pro Pro Glu
690 695 700

Ile Val Ala Gly Leu Asp Glu Leu Ala Leu Ala Thr Glu His Leu Ala
705 710 715 720

Ile Val Asn Arg Ala Ser Trp Asp Ser Phe Leu Lys Ser Phe Ser Arg
725 730 735

Tyr Tyr Thr Asp Phe Lys Ala Ala Val Gln Ala Leu Ala Ala Leu Asp
740 745 750

Cys Leu His Ser Leu Ser Thr Leu Ser Arg Asn Lys Asn Tyr Val Arg
755 760 765

Pro Glu Phe Val Asp Asp Cys Glu Pro Val Glu Ile Asn Ile Gln Ser
770 775 780

Gly Arg His Pro Val Leu Glu Thr Ile Leu Gln Asp Asn Phe Val Pro
785 790 795 800

Asn Asp Thr Ile Leu His Ala Glu Gly Glu Tyr Cys Gln Ile Ile Thr
805 810 815

Gly Pro Asn Met Gly Gly Lys Ser Cys Tyr Ile Arg Gln Val Ala Leu
820 825 830

Ile Ser Ile Met Ala Gln Val Gly Ser Phe Val Pro Ala Ser Phe Ala
835 840 845

Lys Leu His Val Leu Asp Gly Val Phe Thr Arg Met Gly Ala Ser Asp
850 855 860

Ser Ile Gln His Gly Arg Ser Thr Phe Leu Glu Glu Leu Ser Glu Ala
865 870 875 880

Ser His Ile Ile Arg Thr Cys Ser Ser Arg Ser Leu Val Ile Leu Asp
885 890 895

Glu Leu Gly Arg Gly Thr Ser Thr His Asp Gly Val Ala Ile Ala Tyr
900 905 910

Ala Thr Leu Gln His Leu Leu Ala Glu Lys Arg Cys Leu Val Leu Phe
915 920 925

Val Thr His Tyr Pro Glu Ile Ala Glu Ile Ser Asn Gly Phe Pro Gly
930 935 940

Ser Val Gly Thr Tyr His Val Ser Tyr Leu Thr Leu Gln Lys Asp Lys
945 950 955 960

Gly Ser Tyr Asp His Asp Asp Val Thr Tyr Leu Tyr Lys Leu Val Arg
965 970 975

Gly Leu Cys Ser Arg Ser Phe Gly Phe Lys Val Ala Gln Leu Ala Gln
980 985 990

Ile Pro Pro Ser Cys Ile Arg Arg Ala Ile Ser Met Ala Ala Lys Leu
995 1000 1005

Glu Ala Glu Val Arg Ala Arg Glu Arg Asn Thr Arg Met Gly Glu Pro
1010 1015 1020

Glu Gly His Glu Glu Pro Arg Gly Ala Glu Glu Ser Ile Ser Ala Leu
1025 1030 1035 1040

Gly Asp Leu Phe Ala Asp Leu Lys Phe Ala Leu Ser Glu Glu Asp Pro
1045 1050 1055

Trp Lys Ala Phe Glu Phe Leu Lys His Ala Trp Lys Ile Ala Gly Lys
1060 1065 1070

Ile Arg Leu Lys Pro Thr Cys Ser Phe
1075 1080

<210> 20
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<212> DNA
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<220>
<223> MSH6 specific primer 638 for PCR using cDNA of Arabidopsis thaliana

ecotype Columbia

<400> 20

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<210> 21
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Primer S81 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

<400> 21

cgtcgccctt agcatcccc tccttcac 28

<210> 22
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> MSH6 specific primer S823 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

<400> 22

gcttggcgca tctaatacgaa tcatgacagg 30

<210> 23
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> MSH6 specific primer 637 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

<400> 23

gacagcgtca gttcttcaga atgc 24

<210> 24
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> MSH6 specific primer 1S8 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

<400> 24
 atcccggat gcagcgccag agatcgattt tgt 33

<210> 25
 <211> 27
 <212> DNA
 <213> Artificial sequence

<220>
 <223> MSH6 specific primer S83 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

<400> 25
 cgctatatctat ggctgcttcg aattgag 27

<210> 26
 <211> 2188
 <212> DNA
 <213> Arabidopsis thaliana ecotype Columbia
 <223> Clone 43

<400> 26

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| acgaagggtt | tgg | tttccgg | cgat | gct | agc | ggcgg | ggg | gcggc | agg | accacga | 120 | |
| ttaatgtga | agg | aagg | tgct | aaag | gc | acg | ctt | cgt | tgt | tgt | 180 | |
| tctgtcgatg | agg | tttagagg | aac | ggata | ccac | ccgg | aga | gttcc | cg | tcgtgt | 240 | |
| ccgtctggat | tta | agccgc | tga | atccgc | ggt | gat | gctt | cgt | ccct | gtt | 300 | |
| atgcataagt | ttg | aaaagt | cgat | gat | ca | att | ttct | gtt | ccaa | atatt | 360 | |
| gttgttccgc | tga | atgattc | atc | tctatgt | atg | aaagg | cta | atg | atgtt | tat | 420 | |
| cgttccaata | atg | taaaac | tca | agaa | aac | cat | gctt | ttag | tttca | tttca | 480 | |
| gaacttagat | cag | tagaaga | tat | aggag | at | ggc | gat | ttc | tgg | ttt | 540 | |
| gggatgcgtc | cac | tgcttc | tcg | ctt | ga | cg | at | ttct | gg | ttt | 600 | |
| gaggataagg | ttc | ctgttatt | gg | act | ct | aa | agg | ct | gat | ccgg | 660 | |
| tgtggagaga | agaa | agaagt | aa | acgaa | agg | acc | aaat | ttt | gg | ttt | 720 | |
| atcaggatg | cc | aatagaag | ac | gtc | cct | gt | at | ccc | ttt | ttt | 780 | |
| ataccac | ct | g | at | ttt | c | at | aa | at | ttt | ttt | 840 | |
| agtgaatata | tgg | acattgt | gt | ctt | tt | aa | ag | ttt | at | ttt | 900 | |
| ctagatgcgg | aa | tttaggtc | ca | agg | g | act | gg | aa | tg | acc | 960 | |
| aaatgcagac | agg | tttggtat | ct | tgt | aa | at | gg | at | tg | at | 1020 | |
| gctcgtggat | at | aaagg | at | aa | at | at | gg | at | at | at | 1080 | |
| agaggtgcta | at | actataat | tcc | aa | agg | ct | at | tt | at | at | 1140 | |
| agcgagg | aa | acatcg | tg | at | cc | gt | ca | tt | at | ac | 1200 | |
| gagctaca | aa | agt | tt | ca | ac | tgt | tg | ttt | at | ttt | 1260 | |
| ttttgggtt | gg | tccat | cg | at | gt | at | gt | ct | tt | ttt | 1320 | |
| cagg | tt | tct | ca | aa | agg | at | taa | agg | tc | taa | 1380 | |
| gctcta | aa | atatac | g | ac | agg | gt | cc | gg | at | ttt | 1440 | |
| gtaatgg | at | acagat | tg | ct | gg | ag | ttt | gg | at | ttt | 1500 | |
| aaagg | tt | ctg | at | tt | gg | at | aa | at | tt | ttt | 1560 | |
| cttagtgc | tt | ggag | at | tt | at | at | ca | tt | at | ttt | 1620 | |
| aagcatgg | tt | ttt | cc | at | cca | at | ta | gg | tt | ttt | 1680 | |
| acgatgt | aa | at | tt | tg | at | tt | gg | at | tt | ttt | 1740 | |
| tacaaat | at | t | tg | ata | ct | tg | tt | gg | ca | tt | ttt | 1800 |

| | | | | | | |
|-------------|-------------|------------|-------------|-------------|------------|------|
| tgccatccac | tcaaagatgt | agaaagcatc | aataaacggc | ttgatgttagt | tgaagaattc | 1860 |
| acggcaact | cagaaaagtat | gcaaatact | ggccagtatc | tccacaaact | tccagactta | 1920 |
| gaaagactgc | tcggacgc | caagtctagc | gttcgatcat | cagcctctgt | gttgcctgct | 1980 |
| cttctgggaa | aaaaagtgc | gaaacaacga | gttcaaagcat | ttgggcaa | tgtgaaagg | 2040 |
| ttcagaagtgc | gaattgatct | gttgcggct | ctacagaagg | aatcaaataat | gatgagttg | 2100 |
| ctttataaaac | tctgtaaact | tcctatatta | gttagaaaaa | gcgggctaga | gttatttctt | 2160 |
| tctcaattcg | aaggagccat | agatagcg | | | | 2188 |

<210> 27
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 <212> DNA
 <213> Arabidopsis thaliana ecotype Columbia
 <223> Clone 62

<400> 27

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| catttggca | aatttgtaaa | gggttcagaa | gtggaaattga | tctgttgg | gtctcacaga | 120 |
| aggaatcaaa | tatgtatgt | ttgccttata | aactctgtaa | acttcctata | ttatgttagaa | 180 |
| aaagcgggct | agagtttattt | cttctcaat | tcgaagcagc | catagatagc | gactttccaa | 240 |
| attatcagaa | ccaagatgtg | acagatgaaa | acgctgaaaac | tctcacaata | cttatacgaa | 300 |
| tttttatcga | aagagcaact | caatggctcg | aggtcattca | caccataaagc | tgcctagatg | 360 |
| tcctgagatc | ttttgcaatc | gcagcaagtc | tctctgtcg | aagcatggcc | aggcctgtta | 420 |
| tttttcccgaa | atcagaagct | acagatcaga | atcagaaaac | aaaagggcca | atacttaaaa | 480 |
| tccaaggact | atggcatcca | tttgcagttg | cagccgatgg | tcaattgcct | gttccgaatg | 540 |
| ataatactcct | tggcgaggct | agaagaagca | gtggcagcat | tcatcctcg | tcattgttac | 600 |
| tgacgggacc | aaacatgggc | ggaaaatcaa | ctcttctcg | tgcaacatgt | ctggccgtta | 660 |
| tctttggcca | acttggctgc | tacgtccgt | gtgagtcctt | cgaaatctcc | ctcggtgata | 720 |
| ctatctcac | aaggcttggc | gcatctgata | gaatcatgac | aggagagagt | acctttttgg | 780 |
| tagaatgcac | tgagacagcg | tcagttcttc | agaatgcaac | tcaggattca | ctagtaatcc | 840 |
| ttgacgaact | gggcagagga | actagtactt | tcgatggata | cgccattgca | tactcggttt | 900 |
| ttcgtcacct | ggttagagaaa | gttcaatgtc | ggatgtctt | tgcaacacat | taccaccctc | 960 |
| tcacccaagga | attcgcgtct | cacccacgtg | tcacctcgaa | acacatggct | tgcgcattca | 1020 |
| aatcaagatc | tgattatcaa | ccacgtgg | gtgatcaaga | cctagtgttc | ttgtaccgtt | 1080 |
| taaccgaggg | agcttgcct | gagagctacg | gacttcaagt | ggcactcatg | gctgaaatac | 1140 |
| caaaccaagt | ggttggaaaca | gcatcagg | ctgcgtcaagc | catgaagaga | tcaattgggg | 1200 |
| aaaacttcaa | gtcaagtgg | ctaagatctg | agtttc | tctgcgtgaa | gactggctca | 1260 |
| agtcatgtgt | gggttatttct | cgagtcgccc | acaacaatgc | ccccattggc | gaagatgact | 1320 |
| acgacacttt | gttttgccta | tggcatgaga | tcaaatactc | ttactgtgtt | cccaaataaac | 1380 |
| | | | | | ccggg | 1385 |

<210> 28
 <211> 34
 <212> DNA
 <213> Artificial sequence

<220>
 <223> MSH6 specific primer 2S8 for PCR using cDNA of Arabidopsis thaliana
 ecotype Columbia

<400> 28

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<210> 29
 <211> 27
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> MSH6 specific primer S82 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

 <400> 29

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 <212> DNA
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 <223> AtMSH6 full-length cDNA and deduced sequence of the encoded polypeptide

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 tggcgccaaat ctttcccccc tttcgaattt ttcagctca aaacatcgtt tctctctcac 120

 tctctctcac aattccaaaa a atg cag cgc cag aga tcg att ttg tct ttc 171
 Met Gln Arg Gln Arg Ser Ile Leu Ser Phe
 1 5 10

 ttc caa aaa ccc acc gcg gcg act acg aag ggt ttg gtt tcc ggc gat 219
 Phe Gln Lys Pro Thr Ala Ala Thr Thr Lys Gly Leu Val Ser Gly Asp
 15 20 25

 gct gct agc ggc ggg ggc ggc agc gga gga cca cga ttt aat gtg aag 267
 Ala Ala Ser Gly Gly Gly Ser Gly Gly Pro Arg Phe Asn Val Arg
 30 35 40

 gaa ggg gat gct aaa ggc gac gct tct gta cgt ttt gct gtt tcg aaa 315
 Glu Gly Asp Ala Lys Gly Asp Ala Ser Val Arg Phe Ala Val Ser Lys
 45 50 55

 tct gtc gat gag gtt aga gga acg gat act cca ccg gag aag gtt ccg 363
 Ser Val Asp Glu Val Arg Gly Thr Asp Thr Pro Pro Glu Lys Val Pro
 60 65 70

 cgt cgt gtc ctg ccg tct gga ttt aag ccg gct gaa tcc gcc gat 411
 Arg Arg Val Leu Pro Ser Gly Phe Lys Pro Ala Glu Ser Ala Gly Asp
 75 80 85 90

 gct tcg tcc ctg ttc tcc aat att atg cat aag ttt gta aaa gtc gat 459
 Ala Ser Ser Leu Phe Ser Asn Ile Met His Lys Phe Val Lys Val Asp
 95 100 105

gat cga gat tgt tct gga gag agg agc cga gaa gat gtt gtt ccg ctg 507
 Asp Arg Asp Cys Ser Gly Glu Arg Ser Arg Glu Asp Val Val Pro Leu
 110 115 120

aat gat tca tct cta tgt atg aag gct aat gat gtt att cct caa ttt 555
 Asn Asp Ser Ser Leu Cys Met Lys Ala Asn Asp Val Ile Pro Gln Phe
 125 130 135

cgt tcc aat aat ggt aaa act caa gaa aga aac cat gct ttt agt ttc 603
 Arg Ser Asn Asn Gly Lys Thr Gln Glu Arg Asn His Ala Phe Ser Phe
 140 145 150

agt ggg aga gct gaa ctt aga tca gta gaa gat ata gga gta gat ggc 651
 Ser Gly Arg Ala Glu Leu Arg Ser Val Glu Asp Ile Gly Val Asp Gly
 155 160 165 170

gat gtt cct ggt cca gaa aca cca ggg atg cgt cca cgt gct tct cgc 699
 Asp Val Pro Gly Pro Glu Thr Pro Gly Met Arg Pro Arg Ala Ser Arg
 175 180 185

ttg aag cga gtt ctg gag gat gaa atg act ttt aag gag gat aag gtt 747
 Leu Lys Arg Val Leu Glu Asp Glu Met Thr Phe Lys Glu Asp Lys Val
 190 195 200

cct gta ttg gac tct aac aaa agg ctg aaa atg ctc cag gat ccg gtt 795
 Pro Val Leu Asp Ser Asn Lys Arg Leu Lys Met Leu Gln Asp Pro Val
 205 210 215

tgt gga gag aag aaa gaa gta aac gaa gga acc aaa ttt gaa tgg ctt 843
 Cys Gly Glu Lys Lys Glu Val Asn Glu Gly Thr Lys Phe Glu Trp Leu
 220 225 230

gag tct tct cga atc agg gat gcc aat aga aga cgt cct gat gat ccc 891
 Glu Ser Ser Arg Ile Arg Asp Ala Asn Arg Arg Arg Pro Asp Asp Pro
 235 240 245 250

ctt tac gat aga aag acc tta cac ata cca cct gat gtt ttc aag aaa 939
 Leu Tyr Asp Arg Lys Thr Leu His Ile Pro Pro Asp Val Phe Lys Lys
 255 260 265

atg tct gca tca caa aag caa tat tgg agt gtt aag agt gaa tat atg 987
 Met Ser Ala Ser Gln Lys Gln Tyr Trp Ser Val Lys Ser Glu Tyr Met
 270 275 280

gac att gtg ctt ttc ttt aaa gtg ggg aaa ttt tat gag ctg tat gag 1035
 Asp Ile Val Leu Phe Phe Lys Val Gly Lys Phe Tyr Glu Leu Tyr Glu
 285 290 295

cta gat gcg gaa tta ggt cac aag gag ctt gac tgg aag atg acc atg 1083
 Leu Asp Ala Glu Leu Gly His Lys Glu Leu Asp Trp Lys Met Thr Met
 300 305 310

agt ggt gtg gga aaa tgc aga cag gtt ggt atc tct gaa agt ggg ata 1131
 Ser Gly Val Gly Lys Cys Arg Gln Val Gly Ile Ser Glu Ser Gly Ile
 315 320 325 330

gat gag gca gtgcaa aag cta tta qct cgt gga tat aaa gtt gga cga 1179
 Asp Glu Ala Val Gln Lys Leu Leu Ala Arg Gly Tyr Lys Val Gly Arg
 335 340 345

 atc gag cag cta gaa aca tct gac caa gca aaa gcc aga ggt gct aat 1227
 Ile Glu Gln Leu Glu Thr Ser Asp Gln Ala Lys Ala Arg Gly Ala Asn
 350 355 360

 act ata att cca agg aag cta gtt cag gta tta act cca tca aca gca 1275
 Thr Ile Ile Pro Arg Lys Leu Val Gln Val Leu Thr Pro Ser Thr Ala
 365 370 375

 agc gag gga aac atc ggg cct gat gcc gtc cat ctt ctt gct ata aaa 1323
 Ser Glu Gly Asn Ile Gly Pro Asp Ala Val His Leu Leu Ala Ile Lys
 380 385 390

 gag atc aaa atg gag cta caa aag tgt tca act gtg tat gga ttt gct 1371
 Glu Ile Lys Met Glu Leu Gln Lys Cys Ser Thr Val Tyr Gly Phe Ala
 395 400 405 410

 ttt gtt gac tgt gct gcc ttg agg ttt tgg gtt ggg tcc atc agc gat 1419
 Phe Val Asp Cys Ala Ala Leu Arg Phe Trp Val Gly Ser Ile Ser Asp
 415 420 425

 gat gca tca tgt gct ctt gga gcg tta ttg atg cag gtt tct cca 1467
 Asp Ala Ser Cys Ala Ala Leu Gly Ala Leu Leu Met Gln Val Ser Pro
 430 435 440

 aag gaa gtg tta tat gac agt aaa ggg cta tca aga gaa gca caa aag 1515
 Lys Glu Val Leu Tyr Asp Ser Lys Gly Leu Ser Arg Glu Ala Gln Lys
 445 450 455

 gct cta agg aaa tat acg ttg aca ggg tct acg gcg gta cag ttg gct 1563
 Ala Leu Arg Lys Tyr Thr Leu Thr Gly Ser Thr Ala Val Gln Leu Ala
 460 465 470

 cca gta cca caa gta atg ggg gat aca gat gct gct gga gtt aga aat 1611
 Pro Val Pro Gln Val Met Gly Asp Thr Asp Ala Ala Gly Val Arg Asn
 475 480 485 490

 ata ata gaa tct aac gga tac ttt aaa ggt tct tct gaa tca tgg aac 1659
 Ile Ile Glu Ser Asn Gly Tyr Phe Lys Gly Ser Ser Glu Ser Trp Asn
 495 500 505

 tgt gct gtt gat ggt cta aat gaa tgt gat gtt gcc ctt agt gct ctt 1707
 Cys Ala Val Asp Gly Leu Asn Glu Cys Asp Val Ala Leu Ser Ala Leu
 510 515 520

 gga gag cta att aat cat ctg tct agg cta aag cta gaa gat gta ctt 1755
 Gly Glu Leu Ile Asn His Leu Ser Arg Leu Lys Leu Glu Asp Val Leu
 525 530 535

 aag cat ggg gat att ttt cca tac caa gtt tac agg ggt tgt ctc aga 1803
 Lys His Gly Asp Ile Phe Pro Tyr Gln Val Tyr Arg Gly Cys Leu Arg
 540 545 550

 att gat ggc cag acg atg gta aat ctt gag ata ttt aac aat agc tgt 1851

| | | | |
|---|-----|-----|------|
| Ile Asp Gly Gln Thr Met Val Asn Leu Glu Ile Phe Asn Asn Ser Cys | | | |
| 555 | 560 | 565 | 570 |
| gat ggt ggt cct tca ggg acc ttg tac aaa tat ctt gat aac tgt gtt | | | 1899 |
| Asp Gly Gly Pro Ser Gly Thr Leu Tyr Lys Tyr Leu Asp Asn Cys Val | | | |
| 575 | 580 | 585 | |
| agt cca act ggt aag cga ctc tta agg aat tgg atc tgc cat cca ctc | | | 1947 |
| Ser Pro Thr Gly Lys Arg Leu Leu Arg Asn Trp Ile Cys His Pro Leu | | | |
| 590 | 595 | 600 | |
| aaa gat gta gaa agc atc aat aaa cgg ctt gat gta gtt gaa gaa ttc | | | 1995 |
| Lys Asp Val Glu Ser Ile Asn Lys Arg Leu Asp Val Val Glu Glu Phe | | | |
| 605 | 610 | 615 | |
| acg gca aac tca gaa agt atg caa atc act ggc cag tat ctc cac aaa | | | 2043 |
| Thr Ala Asn Ser Glu Ser Met Gln Ile Thr Gly Gln Tyr Leu His Lys | | | |
| 620 | 625 | 630 | |
| ctt cca gac tta gaa aga ctg ctc gga cgc atc aag tct agc gtt cga | | | 2091 |
| Leu Pro Asp Leu Glu Arg Leu Leu Gly Arg Ile Lys Ser Ser Val Arg | | | |
| 635 | 640 | 645 | 650 |
| tca tca gcc tct gtg ttg cct gct ctt ctg ggg aaa aaa gtg ctg aaa | | | 2139 |
| Ser Ser Ala Ser Val Leu Pro Ala Leu Leu Gly Lys Lys Val Leu Lys | | | |
| 655 | 660 | 665 | |
| caa cga gtt aaa gca ttt ggg caa att gtg aaa ggg ttc aga agt gga | | | 2187 |
| Gln Arg Val Lys Ala Phe Gly Gln Ile Val Lys Gly Phe Arg Ser Gly | | | |
| 670 | 675 | 680 | |
| att gat ctg ttg ttg gct cta cag aag gaa tca aat atg atg agt ttg | | | 2235 |
| Ile Asp Leu Leu Leu Ala Leu Gln Lys Glu Ser Asn Met Met Ser Leu | | | |
| 685 | 690 | 695 | |
| ctt tat aaa ctc tgt aaa ctt cct ata tta gta gga aaa agc ggg cta | | | 2283 |
| Leu Tyr Lys Leu Cys Lys Leu Pro Ile Leu Val Gly Lys Ser Gly Leu | | | |
| 700 | 705 | 710 | |
| gag tta ttt ctt tct caa ttc gaa gca gcc ata gat agc gac ttt cca | | | 2331 |
| Glu Leu Phe Leu Ser Gln Phe Glu Ala Ala Ile Asp Ser Asp Phe Pro | | | |
| 715 | 720 | 725 | 730 |
| aat tat cag aac caa gat gtg aca gat gaa aac gct gaa act ctc aca | | | 2379 |
| Asn Tyr Gln Asn Gln Asp Val Thr Asp Glu Asn Ala Glu Thr Leu Thr | | | |
| 735 | 740 | 745 | |
| ata ctt atc gaa ctt ttt atc gaa aga gca act caa tgg tct gag gtc | | | 2427 |
| Ile Leu Ile Glu Leu Phe Ile Glu Arg Ala Thr Gln Trp Ser Glu Val | | | |
| 750 | 755 | 760 | |
| att cac acc ata agc tgc cta gat gtc ctg aga tct ttt gca atc gca | | | 2475 |
| Ile His Thr Ile Ser Cys Leu Asp Val Leu Arg Ser Phe Ala Ile Ala | | | |
| 765 | 770 | 775 | |
| gca agt ctc tct gct gga agc atg gcc agg cct gtt att ttt ccc gaa | | | 2523 |
| Ala Ser Leu Ser Ala Gly Ser Met Ala Arg Pro Val Ile Phe Pro Glu | | | |

| 780 | 785 | 790 | |
|--|------------|------|--------------|
| tca gaa gct aca gat cag aat cag aaa aca aaa ggg cca ata ctt aaa Ser Glu Ala Thr Asp Gln Asn Gln Lys Thr Lys Gly Pro Ile Leu Lys | 795 800 | 805 | 2571 810 |
| atc caa gga cta tgg cat cca ttt gca gtt gca gcc gat ggt caa ttg Ile Gln Gly Leu Trp His Pro Phe Ala Val Ala Ala Asp Gly Gln Leu | 815 | 820 | 2619 825 |
| cct gtt ccg aat gat ata ctc ctt ggc gag gct aga aga agc agt ggc Pro Val Pro Asn Asp Ile Leu Leu Gly Glu Ala Arg Arg Ser Ser Gly | 830 | 835 | 2667 840 |
| agc att cat cct cgg tca ttg tta ctg acg gga cca aac atg ggc gga Ser Ile His Pro Arg Ser Leu Leu Leu Thr Gly Pro Asn Met Gly Gly | 845 | 850 | 2715 855 |
| aaa tca act ctt ctt cgt gca aca tgt ctg gcc gtt atc ttt gcc caa Lys Ser Thr Leu Leu Arg Ala Thr Cys Leu Ala Val Ile Phe Ala Gln | 860 | 865 | 2763 870 |
| ctt ggc tgc tac gtg ccg tgt gag tct tgc gaa atc tcc ctc gtg gat Leu Gly Cys Tyr Val Pro Cys Glu Ser Cys Glu Ile Ser Leu Val Asp | 875 880 | 885 | 2811 890 |
| act atc ttc aca agg ctt ggc gca tct gat aga atc atg aca gga gag Thr Ile Phe Thr Arg Leu Gly Ala Ser Asp Arg Ile Met Thr Gly Glu | 895 | 900 | 2859 905 |
| agt acc ttt ttg gta gaa tgc act gag aca gcg tca gtt ctt cag aat Ser Thr Phe Leu Val Glu Cys Thr Glu Thr Ala Ser Val Leu Gln Asn | 910 | 915 | 2907 920 |
| gca act cag gat tca cta gta atc ctt gac gaa ctg ggc aga gga act Ala Thr Gln Asp Ser Leu Val Ile Leu Asp Glu Leu Gly Arg Gly Thr | 925 | 930 | 2955 935 |
| agt act ttc gat gga tac gcc att gca tac tcg gtt ttt cgt cac ctg Ser Thr Phe Asp Gly Tyr Ala Ile Ala Tyr Ser Val Phe Arg His Leu | 940 | 945 | 3003 950 |
| gta gag aaa gtt caa tgt cgg atg ctc ttt gca aca cat tac cac cct Val Glu Lys Val Gln Cys Arg Met Leu Phe Ala Thr His Tyr His Pro | 955 960 | 965 | 3051 970 |
| ctc acc aag gaa ttc gcg tct cac cca cgt gtc acc tcg aaa cac atg Leu Thr Lys Glu Phe Ala Ser His Pro Arg Val Thr Ser Lys His Met | 975 | 980 | 3099 985 |
| gct tgc gca ttc aaa tca aga tct gat tat caa cca cgt ggt tgt gat Ala Cys Ala Phe Lys Ser Arg Ser Asp Tyr Gln Pro Arg Gly Cys Asp | 990 | 995 | 3147 1000 |
| caa gac cta gtg ttc ttg tac cgt tta acc gag gga gct tgt cct gag Gln Asp Leu Val Phe Leu Tyr Arg Leu Thr Glu Gly Ala Cys Pro Glu | 1005 | 1010 | 3195 1015 |

agc tac gga ctt caa gtg gca ctc atg gct gga ata cca aac caa gtg 3243
Ser Tyr Gly Leu Gln Val Ala Leu Met Ala Gly Ile Pro Asn Gln Val
1020 1025 1030

gtt gaa aca gca tca ggt gct gct caa gcc atg aag aga tca att ggg 3291
Val Glu Thr Ala Ser Gly Ala Ala Gln Ala Met Lys Arg Ser Ile Gly
1035 1040 1045 1050

gga aac ttc aag tca agt gag cta aga tct gag ttc tca agt ctg cat 3339
Glu Asn Phe Lys Ser Ser Glu Leu Arg Ser Glu Phe Ser Ser Leu His
1055 1060 1065

gaa gac tgg ctc aag tca ttg gtg ggt att tct cga gtc gcc cac aac 3387
Glu Asp Trp Leu Lys Ser Leu Val Gly Ile Ser Arg Val Ala His Asn
1070 1075 1080

aat gcc ccc att ggc gaa gat gac tac gac act ttg ttt tgc tta tgg 3435
Asn Ala Pro Ile Gly Glu Asp Asp Tyr Asp Thr Leu Phe Cys Leu Trp
1085 1090 1095

cat gag atc aaa tcc tct tac tgt gtt ccc aaa taaatggcta 3478
His Glu Ile Lys Ser Ser Tyr Cys Val Pro Lys
1100 1105

tgacataaca ctatctgaag ctcgttaagt ctttgccctc tctgatgttt attcctctta 3538
aaaaatgctt atatatcaaa aaattgtttc ctcgattaaa aaaaaaaaaa aaaaaaaaaa 3598
aaaaaaaa 3606

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<223> Polypeptide MSH6

<400> 31

Met Gln Arg Gln Arg Ser Ile Leu Ser Phe Phe Gln Lys Pro Thr Ala
1 5 10 15

Ala Thr Thr Lys Gly Leu Val Ser Gly Asp Ala Ala Ser Gly Gly Gly
20 25 30

Gly Ser Gly Gly Pro Arg Phe Asn Val Arg Glu Gly Asp Ala Lys Gly
35 40 45

Asp Ala Ser Val Arg Phe Ala Val Ser Lys Ser Val Asp Glu Val Arg
50 55 60

Gly Thr Asp Thr Pro Pro Glu Lys Val Pro Arg Arg Val Leu Pro Ser
65 70 75 80

Gly Phe Lys Pro Ala Glu Ser Ala Gly Asp Ala Ser Ser Leu Phe Ser
85 90 95

Asn Ile Met His Lys Phe Val Lys Val Asp Asp Arg Asp Cys Ser Gly

100 105 110

Glu Arg Ser Arg Glu Asp Val Val Pro Leu Asn Asp Ser Ser Leu Cys
115 120 125

Met Lys Ala Asn Asp Val Ile Pro Gln Phe Arg Ser Asn Asn Gly Lys
130 135 140

Thr Gln Glu Arg Asn His Ala Phe Ser Phe Ser Gly Arg Ala Glu Leu
145 150 155 160

Arg Ser Val Glu Asp Ile Gly Val Asp Gly Asp Val Pro Gly Pro Glu
165 170 175

Thr Pro Gly Met Arg Pro Arg Ala Ser Arg Leu Lys Arg Val Leu Glu
180 185 190

Asp Glu Met Thr Phe Lys Glu Asp Lys Val Pro Val Leu Asp Ser Asn
195 200 205

Lys Arg Leu Lys Met Leu Gln Asp Pro Val Cys Gly Glu Lys Lys Glu
210 215 220

Val Asn Glu Gly Thr Lys Phe Glu Trp Leu Glu Ser Ser Arg Ile Arg
225 230 235 240

Asp Ala Asn Arg Arg Pro Asp Asp Pro Leu Tyr Asp Arg Lys Thr
245 250 255

Leu His Ile Pro Pro Asp Val Phe Lys Lys Met Ser Ala Ser Gln Lys
260 265 270

Gln Tyr Trp Ser Val Lys Ser Glu Tyr Met Asp Ile Val Leu Phe Phe
275 280 285

Lys Val Gly Lys Phe Tyr Glu Leu Tyr Glu Leu Asp Ala Glu Leu Gly
290 295 300

His Lys Glu Leu Asp Trp Lys Met Thr Met Ser Gly Val Gly Lys Cys
305 310 315 320

Arg Gln Val Gly Ile Ser Glu Ser Gly Ile Asp Glu Ala Val Gln Lys
325 330 335

Leu Leu Ala Arg Gly Tyr Lys Val Gly Arg Ile Glu Gln Leu Glu Thr
340 345 350

Ser Asp Gln Ala Lys Ala Arg Gly Ala Asn Thr Ile Ile Pro Arg Lys
355 360 365

Leu Val Gln Val Leu Thr Pro Ser Thr Ala Ser Glu Gly Asn Ile Gly
370 375 380

Pro Asp Ala Val His Leu Leu Ala Ile Lys Glu Ile Lys Met Glu Leu
385 390 395 400

Gln Lys Cys Ser Thr Val Tyr Gly Phe Ala Phe Val Asp Cys Ala Ala

405 410 415

Leu Arg Phe Trp Val Gly Ser Ile Ser Asp Asp Ala Ser Cys Ala Ala
420 425 430

Leu Gly Ala Leu Leu Met Gln Val Ser Pro Lys Glu Val Leu Tyr Asp
435 440 445

Ser Lys Gly Leu Ser Arg Glu Ala Gln Lys Ala Leu Arg Lys Tyr Thr
450 455 460

Leu Thr Gly Ser Thr Ala Val Gln Leu Ala Pro Val Pro Gln Val Met
465 470 475 480

Gly Asp Thr Asp Ala Ala Gly Val Arg Asn Ile Ile Glu Ser Asn Gly
485 490 495

Tyr Phe Lys Gly Ser Ser Glu Ser Trp Asn Cys Ala Val Asp Gly Leu
500 505 510

Asn Glu Cys Asp Val Ala Leu Ser Ala Leu Gly Glu Leu Ile Asn His
515 520 525

Leu Ser Arg Leu Lys Leu Glu Asp Val Leu Lys His Gly Asp Ile Phe
530 535 540

Pro Tyr Gln Val Tyr Arg Gly Cys Leu Arg Ile Asp Gly Gln Thr Met
545 550 555 560

Val Asn Leu Glu Ile Phe Asn Asn Ser Cys Asp Gly Gly Pro Ser Gly
565 570 575

Thr Leu Tyr Lys Tyr Leu Asp Asn Cys Val Ser Pro Thr Gly Lys Arg
580 585 590

Leu Leu Arg Asn Trp Ile Cys His Pro Leu Lys Asp Val Glu Ser Ile
595 600 605

Asn Lys Arg Leu Asp Val Val Glu Glu Phe Thr Ala Asn Ser Glu Ser
610 615 620

Met Gln Ile Thr Gly Gln Tyr Leu His Lys Leu Pro Asp Leu Glu Arg
625 630 635 640

Leu Leu Gly Arg Ile Lys Ser Ser Val Arg Ser Ser Ala Ser Val Leu
645 650 655

Pro Ala Leu Leu Gly Lys Lys Val Leu Lys Gln Arg Val Lys Ala Phe
660 665 670

Gly Gln Ile Val Lys Gly Phe Arg Ser Gly Ile Asp Leu Leu Leu Ala
675 680 685

Leu Gln Lys Glu Ser Asn Met Met Ser Leu Leu Tyr Lys Leu Cys Lys
690 695 700

Leu Pro Ile Leu Val Gly Lys Ser Gly Leu Glu Leu Phe Leu Ser Gln

705 710 715 720
Phe Glu Ala Ala Ile Asp Ser Asp Phe Pro Asn Tyr Gln Asn Gln Asp
725 730 735
Val Thr Asp Glu Asn Ala Glu Thr Leu Thr Ile Leu Ile Glu Leu Phe
740 745 750
Ile Glu Arg Ala Thr Gln Trp Ser Glu Val Ile His Thr Ile Ser Cys
755 760 765
Leu Asp Val Leu Arg Ser Phe Ala Ile Ala Ala Ser Leu Ser Ala Gly
770 775 780
Ser Met Ala Arg Pro Val Ile Phe Pro Glu Ser Glu Ala Thr Asp Gln
785 790 795 800
Asn Gln Lys Thr Lys Gly Pro Ile Leu Lys Ile Gln Gly Leu Trp His
805 810 815
Pro Phe Ala Val Ala Ala Asp Gly Gln Leu Pro Val Pro Asn Asp Ile
820 825 830
Leu Leu Gly Glu Ala Arg Arg Ser Ser Gly Ser Ile His Pro Arg Ser
835 840 845
Leu Leu Leu Thr Gly Pro Asn Met Gly Gly Lys Ser Thr Leu Leu Arg
850 855 860
Ala Thr Cys Leu Ala Val Ile Phe Ala Gln Leu Gly Cys Tyr Val Pro
865 870 875 880
Cys Glu Ser Cys Glu Ile Ser Leu Val Asp Thr Ile Phe Thr Arg Leu
885 890 895
Gly Ala Ser Asp Arg Ile Met Thr Gly Glu Ser Thr Phe Leu Val Glu
900 905 910
Cys Thr Glu Thr Ala Ser Val Leu Gln Asn Ala Thr Gln Asp Ser Leu
915 920 925
Val Ile Leu Asp Glu Leu Gly Arg Gly Thr Ser Thr Phe Asp Gly Tyr
930 935 940
Ala Ile Ala Tyr Ser Val Phe Arg His Leu Val Glu Lys Val Gln Cys
945 950 955 960
Arg Met Leu Phe Ala Thr His Tyr His Pro Leu Thr Lys Glu Phe Ala
965 970 975
Ser His Pro Arg Val Thr Ser Lys His Met Ala Cys Ala Phe Lys Ser
980 985 990
Arg Ser Asp Tyr Gln Pro Arg Gly Cys Asp Gln Asp Leu Val Phe Leu
995 1000 1005
Tyr Arg Leu Thr Glu Gly Ala Cys Pro Glu Ser Tyr Gly Leu Gln Val

1010 1015 1020

Ala Leu Met Ala Gly Ile Pro Asn Gln Val Val Glu Thr Ala Ser Gly
1025 1030 1035 1040

Ala Ala Gln Ala Met Lys Arg Ser Ile Gly Glu Asn Phe Lys Ser Ser
1045 1050 1055

Glu Leu Arg Ser Glu Phe Ser Ser Leu His Glu Asp Trp Leu Lys Ser
1060 1065 1070

Leu Val Gly Ile Ser Arg Val Ala His Asn Asn Ala Pro Ile Gly Glu
1075 1080 1085

Asp Asp Tyr Asp Thr Leu Phe Cys Leu Trp His Glu Ile Lys Ser Ser
1090 1095 1100

Tyr Cys Val Pro Lys
1105

<210> 32
<211> 24
<212> DNA
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<220>
<223> Forward primer for PCR amplification of ATHGENEA microsatellite

<400> 32

accatgcata gcttaaactt cttg 24

<210> 33
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse primer for PCR amplification of ATHGENEA microsatellite

<400> 33

acataaccac aaataggggt gc 22

<210> 34
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer DMCIN-A for PCR on genomic DNA of Arabidopsis thaliana
ssp. Landsberg erecta "Ler"

<400> 34

gaagcgatat tgttcgtg 18

<210> 35
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse primer DMCIN-B for PCR on genomic DNA of Arabidopsis thaliana ssp. Landsberg erecta "Ler"

<400> 35

agattgcgag aacattcc 18

<210> 36
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer DMCIN-1 for PCR on genomic DNA of Arabidopsis thaliana ssp. Landsberg erecta "Ler"

<400> 36

acgcgtcgac tcagctatga gattactcgt g 31

<210> 37
<211> 29
<212> DNA
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<220>
<223> Reverse primer DMCIN-2 for PCR on genomic DNA of Arabidopsis thaliana ssp. Landsberg erecta "Ler"

<400> 37

gctctagatt tctcgctcta agactctct 29

<210> 38
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer DMCIN-3 for PCR on genomic DNA of Arabidopsis thaliana ssp. Landsberg erecta "Ler"

<400> 38

gctctagagc ttctcttaag taagtgattt at 32

<210> 39
<211> 48
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse primer DMCIN-4 for PCR on genomic DNA of *Arabidopsis thaliana* ssp. *Landsberg erecta* "Ler"

<400> 39

tccccccgggc tcgagagatc tccatggttt cttcagctct atgaatcc 48

<210> 40
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer DMCl_a for PCR on genomic DNA of *Arabidopsis thaliana* ssp. *Landsberg erecta* "Ler"

<400> 40

acgcgtcgac gaattcgcaa gtgggg 26

<210> 41
<211> 38
<212> DNA
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<220>
<223> Reverse primer DMC1b for PCR on genomic DNA of *Arabidopsis thaliana* ssp. *Landsberg erecta* "Ler"

<400> 41

tccatggaga tctccgggt accgatttgc ttcgaggg 38

<210> 42
<211> 20
<212> DNA
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<220>
<223> Forward primer for PCR amplification of ATEAT1 SSLP marker in *Arabidopsis thaliana* subspecies

<400> 42

gccactgcgt gaatgatatg 20

<210> 43
<211> 22
<212> DNA
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<220>
<223> Reverse primer for PCR amplification of ATEAT1 SSLP marker in Arabidopsis thaliana subspecies

<400> 43

cgaacagcca acattaattc cc 22

<210> 44
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer for PCR amplification of NGA63 SSLP marker in Arabidopsis thaliana subspecies

<400> 44

aaccaaggca cagaagcg 18

<210> 45
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse primer for PCR amplification of NGA63 SSLP marker in Arabidopsis thaliana subspecies

<400> 45

acccaagtga tcgccacc 18

<210> 46
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies

<400> 46

taccgaacca aaacacaaaag g 21

<210> 47

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Reverse primer for PCR amplification of NGA248 SSLP marker in
Arabidopsis thaliana subspecies

<400> 47

tctgtatctc ggtgaattct cc 22

<210> 48

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Forward primer for PCR amplification of NGA128 SSLP marker in
Arabidopsis thaliana subspecies

<400> 48

ggtctgttga tgcgttaagt cg 22

<210> 49

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Reverse primer for PCR amplification of NGA128 SSLP marker in
Arabidopsis thaliana subspecies

<400> 49

atcttgaaac cttagggag gg 22

<210> 50

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Forward primer for PCR amplification of NGA280 SSLP marker in
Arabidopsis thaliana subspecies

<400> 50

ctgatctcac ggacaatagt gc 22

<210> 51
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse primer for PCR amplification of NGA280 SSLP marker in Arabidopsis thaliana subspecies

<400> 51

ggctccataaa aaagtgcacc 20

<210> 52
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<212> DNA
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<220>
<223> Forward primer for PCR amplification of NGA111 SSLP marker in Arabidopsis thaliana subspecies

<400> 52

ctccagttgg aagctaaagg g 21

<210> 53
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<212> DNA
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<220>
<223> Reverse primer for PCR amplification of NGA111 SSLP marker in Arabidopsis thaliana subspecies

<400> 53

tgttttttag gacaaatggc g 21

<210> 54
<211> 20
<212> DNA
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<220>
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<400> 54

ccttcacatc caaaacccac 20

<210> 55
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse primer for PCR amplification of NGA168 SSLP marker in Arabidopsis thaliana subspecies

<400> 55

gcacataccca acaaccagaa 20

<210> 56
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer for PCR amplification of NGA1126 SSLP marker in Arabidopsis thaliana subspecies

<400> 56

cgctacgctt ttccggtaaag 20

<210> 57
<211> 20
<212> DNA
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<220>
<223> Reverse primer for PCR amplification of NGA1126 SSLP marker in Arabidopsis thaliana subspecies

<400> 57

gcacagtcca agtcacaacc 20

<210> 58
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer for PCR amplification of NGA361 SSLP marker in Arabidopsis thaliana subspecies

<400> 58

aaagagatga gaatttggac 20

<210> 59
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse primer for PCR amplification of NGA361 SSLP marker in
Arabidopsis thaliana subspecies

<400> 59

acatatcaat atattaaagt agc 23

<210> 60
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer for PCR amplification of NGA168 SSLP marker in
Arabidopsis thaliana subspecies

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tctgttactg cactgccg 18

<210> 61
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<212> DNA
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<220>
<223> Reverse primer for PCR amplification of NGA168 SSLP marker in
Arabidopsis thaliana subspecies

<400> 61

gaggacatgt ataggagcct cg 22

<210> 62
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer for PCR amplification of AthB102 SSLP marker in
Arabidopsis thaliana subspecies

<400> 62

tgacctccctc ttccatggag 20

<210> 63
<211> 22
<212> DNA
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<220>
<223> Reverse primer for PCR amplification of AthBIO2 SSLP marker in
Arabidopsis thaliana subspecies

<400> 63

ttaacagaaa cccaaagctt tc 22

<210> 64
<211> 21
<212> DNA
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<220>
<223> Forward primer for PCR amplification of AthUBIQUE SSLP marker in
Arabidopsis thaliana subspecies

<400> 64

aggcaaatgt ccatttcatt g 21

<210> 65
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<220>
<223> Reverse primer for PCR amplification of AthUBIQUE SSLP marker in
Arabidopsis thaliana subspecies

<400> 65

acgacatggc agatttctcc 20

<210> 66
<211> 21
<212> DNA
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<220>
<223> Forward primer for PCR amplification of NGA172 SSLP marker in
Arabidopsis thaliana subspecies

<400> 66

agctgcttcc ttatacgctc c 21

<210> 67
<211> 19
<212> DNA
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<220>
<223> Reverse primer for PCR amplification of NGA172 SSLP marker in Arabidopsis thaliana subspecies

<400> 67

catccgaatg ccattgttc 19

<210> 68
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer for PCR amplification of NGA126 SSLP marker in Arabidopsis thaliana subspecies

<400> 68

aaaaaaacgc tactttcgtg g 21

<210> 69
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse primer for PCR amplification of NGA126 SSLP marker in Arabidopsis thaliana subspecies

<400> 69

caagagcaat atcaagagca gc 22

<210> 70
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer for PCR amplification of NGA162 SSLP marker in Arabidopsis thaliana subspecies

<400> 70

catgcaattt gcatctgagg 20

<210> 71

<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse primer for PCR amplification of NGA162 SSLP marker in
Arabidopsis thaliana subspecies

<400> 71

ctctgtcaact cttttcctct gg 22

<210> 72
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer for PCR amplification of NGA6 SSLP marker in
Arabidopsis
thaliana subspecies

<400> 72

tggatttctt cctctttca c 21

<210> 73
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse primer for PCR amplification of NGA6 SSLP marker in
Arabidopsis
thaliana subspecies

<400> 73

atggagaagc ttacactgat c 21

<210> 74
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer for PCR amplification of NGA12 SSLP marker in
Arabidopsis
thaliana subspecies

<400> 74

aatgttgtcc tcccccttcctc 20

<210> 75
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse primer for PCR amplification of NGA12 SSLP marker in
Arabidopsis
thaliana subspecies

<400> 75

tgatgctctc tgaaacaaga gc 22

<210> 76
<211> 21
<212> DNA
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Arabidopsis
thaliana subspecies

<400> 76

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<210> 77
<211> 22
<212> DNA
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Arabidopsis
thaliana subspecies

<400> 77

tggctttcgt ttataaacat cc 22

<210> 78
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Arabidopsis thaliana subspecies

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gcgaaaaaac aaaaaaatcc a 21

<210> 79
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cgacgaatcg acagaattag g 21

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gaaatccaaa tcccagagag g 21

<210> 81
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tctccccact agttttgtgt cc 22

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<400> 82

taccgtcaat ttcatcgcc 19

<210> 83
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<220>
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Arabidopsis thaliana subspecies

<400> 83

ggatccctaa ctgtaaaatc cc 22

<210> 84
<211> 22
<212> DNA
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<220>
<223> Forward primer for PCR amplification of CA72 SSLP marker in
Arabidopsis
thaliana subspecies

<400> 84

aatcccagta accaaacaca ca 22

<210> 85
<211> 20
<212> DNA
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<220>
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Arabidopsis
thaliana subspecies

<400> 85

cccagtctaa ccacgaccac 20

<210> 86
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Arabidopsis thaliana subspecies

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gttttggaa gtttgctgg 20

<210> 87
<211> 24
<212> DNA
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<210> 88
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<400> 88

gttatggagt ttcttagggca cg 22

<210> 89
<211> 20
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tgcggccattt tggttcttctc 20

<210> 90
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<212> DNA
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<210> 91
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<400> 91

ggtttcgttt cactatccag g 21

<210> 92
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<400> 92

ggagaaaaatg tcactctcca cc 22

<210> 93
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<400> 93

aggcatggga gacatttacg 20

<210> 94
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<212> DNA
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<400> 94

ctccaccaat catgcaaatg 20

<210> 95
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Arabidopsis thaliana subspecies

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tcaggaggaa ctaaagttag gg 22

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Arabidopsis thaliana subspecies

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cacactgaag atggtcttga gg 22

<210> 98
<211> 8062
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<213> Arabidopsis thaliana ecotype Columbia

<220>
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aagaaatgaa agatatatat tttttttca ttatcaaac aaaacaacaa gactttttt 120

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| ttttacccct aagtttaaca cctagaacct tctccatctt cgcaagcaca gcctgattag | 240 |
| gaacagctt accattctca tattcctgaa ctacctgagt cctctcattt atctgttcg | 300 |
| ccaaatccgc ttgtgacatc ttcttcctcca atctcgctt ctgtatcatc aacctcacct | 360 |
| ctgctttcac acgatccatc gccgcaggct ctgttcttc ttccagcttc ttcgtgttaa | 420 |
| tcaccggAAC cgccgttagat ttccccttt tggtcaacc ggcatcgaa ttcttaaccg | 480 |
| tttgaaccgc gacaccgtt ctcagagctg cgtaaccgc ttccggatcg cgtaggtctt | 540 |
| ggctcttttg ttttgattt gggagaacta ctggttccca gtcttgcgtt actgctcctg | 600 |
| ggtatctgct cgccatcgatc gatgaattga gagaaggaa caacgcgaaa attttattaa | 660 |
| tctgagttt gaaattgaga aacgatgaag atgaagaatg ttgttgagag gatttgata | 720 |
| tttatatatata cgaagattgg ttctggaga attcgatcat cttttctcc attttcgat | 780 |
| ctggAACGTT cttagagatg attgacgacg tgcattatc tgatttgcag ttaaccatg | 840 |
| cttttgggt tggattcgat gtacaccata ttatccgatt tggctcaatg gttttatata | 900 |
| aatttgggtt tcggttcggt tatgagttt cattaaaatt aagctaacc aaaaatttcg | 960 |
| taaaattttat ttccgggttca attcggatcc cttacttcca gaaccgaatt attcgaaacc | 1020 |
| ggggtagcc gaaccgaata ccaatgcctg attgactcg tggctagaaa gatccaaacgg | 1080 |
| tatacaataa tagaacataa atcggacggt catcaaagcc tcaaagagtg aacagtcaac | 1140 |
| aaaaaaagt gggccctgag gagtacgtt tccgcattt ctacgacgca aggcggaaat | 1200 |
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| cactctctc cacaatttcca aaaaatgcag cgccagagat cgattttgtc ttcttccaa | 1320 |
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| ggcagccgg accacgattt aatgtgaagg aagggatgc taaaggcgac gtttctgtac | 1440 |
| gttttgcgtt ttccgaaatct gtcgtgagg ttagaggaac ggatactcca cgggagaagg | 1500 |
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| ttagtttcag tggagagct gaacttagat cagtagaaga tataggagta gatggcgatg | 1920 |
| ttcctggtcc agaaacacca gggatgcgtc cacgtcgttcc tcgcttgaag cgagttctgg | 1980 |
| aggatgaaat gactttaag gaggataagg ttcctgtatt ggactctaacc aaaaggctga | 2040 |
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Gln Pro Thr Ile Ser Arg Phe Phe Lys Lys Ala Val Lys Ser Glu Leu
35 40 45
Thr His Lys Gln Glu Gln Glu Val Ala Val Gly Asn Gly Ala Gly Ser
50 55 60
Glu Ser Ile Cys Leu Asp Thr Asp Glu Glu Asp Asn Leu Ser Ser Val
65 70 75 80
Ala Ser Thr Thr Val Thr Asn Asp Ser Phe Pro Leu Lys Gly Ser Val
85 90 95
Ser Ser Lys Asn Ser Lys Asn Ser Glu Lys Thr Ser Gly Thr Ser Thr
100 105 110
Thr Phe Asn Asp Ile Asp Phe Ala Lys Lys Leu Asp Arg Ile Met Lys
115 120 125
Arg Arg Ser Asp Glu Asn Val Glu Ala Glu Asp Asp Glu Glu Glu Gly
130 135 140
Glu Glu Asp Phe Val Lys Lys Ala Arg Lys Ser Pro Thr Ala Lys
145 150 155 160
Leu Thr Pro Leu Asp Lys Gln Val Lys Asp Leu Lys Met His His Arg
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Asp Lys Val Leu Val Ile Arg Val Gly Tyr Lys Tyr Lys Cys Phe Ala
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Glu Asp Ala Val Thr Val Ser Arg Ile Leu His Ile Lys Leu Val Pro
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Gln Phe Ala Tyr Cys Ser Phe Pro Asp Val Arg Leu Asn Val His Leu
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Glu Arg Leu Val His His Asn Leu Lys Val Ala Val Val Glu Gln Ala
245 250 255
Glu Thr Ser Ala Ile Lys Lys His Asp Pro Gly Ala Ser Lys Ser Ser
260 265 270
Val Phe Glu Arg Lys Ile Ser Asn Val Phe Thr Lys Ala Thr Phe Gly
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Asn Ser Ile Trp Ala Leu Ser Arg Asp Val His Gln Gly Lys Val Ala
305 310 315 320
Lys Tyr Ser Leu Ile Ser Val Asn Leu Asn Asn Gly Glu Val Val Tyr
325 330 335

Asp Glu Phe Glu Glu Pro Asn Leu Ala Asp Glu Lys Leu Gln Ile Arg
340 345 350
Ile Lys Tyr Leu Gln Pro Ile Glu Val Leu Val Asn Thr Asp Asp Leu
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Pro Leu His Val Ala Lys Phe Phe Lys Asp Ile Ser Cys Pro Leu Ile
370 375 380
His Lys Gln Glu Tyr Asp Leu Glu Asp His Val Val Gln Ala Ile Lys
385 390 395 400
Val Met Asn Glu Lys Ile Gln Leu Ser Pro Ser Leu Ile Arg Leu Val
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Ser Lys Leu Tyr Ser His Met Val Glu Tyr Asn Asn Glu Gln Val Met
420 425 430
Leu Ile Pro Ser Ile Tyr Ser Pro Phe Ala Ser Lys Ile His Met Leu
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Leu Asp Pro Asn Ser Leu Gln Ser Leu Asp Ile Phe Thr His Asp Gly
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Gly Lys Gly Ser Leu Phe Trp Leu Leu Asp His Thr Arg Thr Ser Phe
465 470 475 480
Gly Leu Arg Met Leu Arg Glu Trp Ile Leu Lys Pro Leu Val Asp Val
485 490 495
His Gln Ile Glu Glu Arg Leu Asp Ala Ile Glu Cys Ile Thr Ser Glu
500 505 510
Ile Asn Asn Ser Ile Phe Phe Glu Ser Leu Asn Gln Met Leu Asn His
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Thr Pro Asp Leu Leu Arg Thr Leu Asn Arg Ile Met Tyr Gly Thr Thr
530 535 540
Ser Arg Lys Glu Val Tyr Phe Tyr Leu Lys Gln Ile Thr Ser Phe Val
545 550 555 560
Asp His Phe Lys Met His Gln Ser Tyr Leu Ser Glu His Phe Lys Ser
565 570 575
Ser Asp Gly Arg Ile Gly Lys Gln Ser Pro Leu Leu Phe Arg Leu Phe
580 585 590
Ser Glu Leu Asn Glu Leu Leu Ser Thr Thr Gln Leu Pro His Phe Leu
595 600 605
Thr Met Ile Asn Val Ser Ala Val Met Glu Lys Asn Ser Asp Lys Gln
610 615 620
Val Met Asp Phe Phe Asn Leu Asn Asn Tyr Asp Cys Ser Glu Gly Ile
625 630 635 640
Ile Lys Ile Gln Arg Glu Ser Glu Ser Val Arg Ser Gln Leu Lys Glu
645 650 655
Glu Leu Ala Glu Ile Arg Lys Tyr Leu Lys Arg Pro Tyr Leu Asn Phe
660 665 670
Arg Asp Glu Val Asp Tyr Leu Ile Glu Val Lys Asn Ser Gln Ile Lys
675 680 685
Asp Leu Pro Asp Asp Trp Ile Lys Val Asn Asn Thr Lys Met Val Ser
690 695 700
Arg Phe Thr Thr Pro Arg Thr Gln Lys Leu Thr Gln Lys Leu Glu Tyr
705 710 715 720
Tyr Lys Asp Leu Leu Ile Arg Glu Ser Glu Leu Gln Tyr Lys Glu Phe
725 730 735
Leu Asn Lys Ile Thr Ala Glu Tyr Thr Glu Leu Arg Lys Ile Thr Leu
740 745 750
Asn Leu Ala Gln Tyr Asp Cys Ile Leu Ser Leu Ala Ala Thr Ser Cys
755 760 765
Asn Val Asn Tyr Val Arg Pro Thr Phe Val Asn Gly Gln Gln Ala Ile
770 775 780
Ile Ala Lys Asn Ala Arg Asn Pro Ile Ile Glu Ser Leu Asp Val His

| | | | |
|---|------|------|------|
| 785 | 790 | 795 | 800 |
| Tyr Val Pro Asn Asp Ile Met Met Ser Pro Glu Asn Gly Lys Ile Asn | | | |
| 805 | 810 | 815 | |
| Ile Ile Thr Gly Pro Asn Met Gly Gly Lys Ser Ser Tyr Ile Arg Gln | | | |
| 820 | 825 | 830 | |
| Val Ala Leu Leu Thr Ile Met Ala Gln Ile Gly Ser Phe Val Pro Ala | | | |
| 835 | 840 | 845 | |
| Glu Glu Ile Arg Leu Ser Ile Phe Glu Asn Val Leu Thr Arg Ile Gly | | | |
| 850 | 855 | 860 | |
| Ala His Asp Asp Ile Ile Asn Gly Asp Ser Thr Phe Lys Val Glu Met | | | |
| 865 | 870 | 875 | 880 |
| Leu Asp Ile Leu His Ile Leu Lys Asn Cys Asn Lys Arg Ser Leu Leu | | | |
| 885 | 890 | 895 | |
| Leu Leu Asp Glu Val Gly Arg Gly Thr Gly Thr His Asp Gly Ile Ala | | | |
| 900 | 905 | 910 | |
| Ile Ser Tyr Ala Leu Ile Lys Tyr Phe Ser Glu Leu Ser Asp Cys Pro | | | |
| 915 | 920 | 925 | |
| Leu Ile Leu Phe Thr Thr His Phe Pro Met Leu Gly Glu Ile Lys Ser | | | |
| 930 | 935 | 940 | |
| Pro Leu Ile Arg Asn Tyr His Met Asp Tyr Val Glu Glu Gln Lys Thr | | | |
| 945 | 950 | 955 | 960 |
| Gly Glu Asp Trp Met Ser Val Ile Phe Leu Tyr Lys Leu Lys Lys Gly | | | |
| 965 | 970 | 975 | |
| Leu Thr Tyr Asn Ser Tyr Gly Met Asn Val Ala Lys Leu Ala Arg Leu | | | |
| 980 | 985 | 990 | |
| Asp Lys Asp Ile Ile Asn Arg Ala Phe Ser Ile Ser Glu Glu Leu Arg | | | |
| 995 | 1000 | 1005 | |
| Lys Glu Ser Ile Asn Glu Asp Ala Leu Lys Leu Phe Ser Ser Leu Lys | | | |
| 1010 | 1015 | 1020 | |
| Arg Ile Leu Lys Ser Asp Asn Ile Thr Ala Thr Asp Lys Leu Ala Lys | | | |
| 1025 | 1030 | 1035 | 1040 |
| Leu Leu Ser Leu Asp Ile His | | | |
| 1045 | | | |

<210> 103
<211> 1242
<212> PRT
<213> *Saccharomyces cerevisiae*

| | | | |
|---|-----|-----|----|
| <400> 103 | | | |
| Met Ala Pro Ala Thr Pro Lys Thr Ser Lys Thr Ala His Phe Glu Asn | | | |
| 1 | 5 | 10 | 15 |
| Gly Ser Thr Ser Ser Gln Lys Lys Met Lys Gln Ser Ser Leu Leu Ser | | | |
| 20 | 25 | 30 | |
| Phe Phe Ser Lys Gln Val Pro Ser Gly Thr Pro Ser Lys Lys Val Gln | | | |
| 35 | 40 | 45 | |
| Lys Pro Thr Pro Ala Thr Leu Glu Asn Thr Ala Thr Asp Lys Ile Thr | | | |
| 50 | 55 | 60 | |
| Lys Asn Pro Gln Gly Gly Lys Thr Gly Lys Leu Phe Val Asp Val Asp | | | |
| 65 | 70 | 75 | 80 |
| Glu Asp Asn Asp Leu Thr Ile Ala Glu Glu Thr Val Ser Thr Val Arg | | | |
| 85 | 90 | 95 | |
| Ser Asp Ile Met His Ser Gln Glu Pro Gln Ser Asp Thr Met Leu Asn | | | |
| 100 | 105 | 110 | |
| Ser Asn Thr Thr Glu Pro Lys Ser Thr Thr Asp Glu Asp Leu Ser | | | |
| 115 | 120 | 125 | |

Ser Ser Gln Ser Arg Arg Asn His Lys Arg Arg Val Asn Tyr Ala Glu
130 135 140
Ser Asp Asp Asp Asp Ser Asp Thr Thr Phe Thr Ala Lys Arg Lys Lys
145 150 155 160
Gly Lys Val Val Asp Ser Glu Ser Asp Glu Asp Glu Tyr Leu Pro Asp
165 170 175
Lys Asn Asp Gly Asp Glu Asp Asp Ile Ala Asp Asp Lys Glu Asp
180 185 190
Ile Lys Gly Glu Leu Ala Glu Asp Ser Gly Asp Asp Asp Asp Leu Ile
195 200 205
Ser Leu Ala Glu Thr Thr Ser Lys Lys Lys Phe Ser Tyr Asn Thr Ser
210 215 220
His Ser Ser Ser Pro Phe Thr Arg Asn Ile Ser Arg Asp Asn Ser Lys
225 230 235 240
Lys Lys Ser Arg Pro Asn Gln Ala Pro Ser Arg Ser Tyr Asn Pro Ser
245 250 255
His Ser Gln Pro Ser Ala Thr Ser Lys Ser Ser Lys Phe Asn Lys Gln
260 265 270
Asn Glu Glu Arg Tyr Gln Trp Leu Val Asp Glu Arg Asp Ala Gln Arg
275 280 285
Arg Pro Lys Ser Asp Pro Glu Tyr Asp Pro Arg Thr Leu Tyr Ile Pro
290 295 300
Ser Ser Ala Trp Asn Lys Phe Thr Pro Phe Glu Lys Gln Tyr Trp Glu
305 310 315 320
Ile Lys Ser Lys Met Trp Asp Cys Ile Val Phe Phe Lys Lys Gly Lys
325 330 335
Phe Phe Glu Leu Tyr Glu Lys Asp Ala Leu Leu Ala Asn Ala Leu Phe
340 345 350
Asp Leu Lys Ile Ala Gly Gly Arg Ala Asn Met Gln Leu Ala Gly
355 360 365
Ile Pro Glu Met Ser Phe Glu Tyr Trp Ala Ala Gln Phe Ile Gln Met
370 375 380
Gly Tyr Lys Val Ala Lys Val Asp Gln Arg Glu Ser Met Leu Ala Lys
385 390 395 400
Glu Met Arg Glu Gly Ser Lys Gly Ile Val Lys Arg Glu Leu Gln Cys
405 410 415
Ile Leu Thr Ser Gly Thr Leu Thr Asp Gly Asp Met Leu His Ser Asp
420 425 430
Leu Ala Thr Phe Cys Leu Ala Ile Arg Glu Glu Pro Gly Asn Phe Tyr
435 440 445
Asn Glu Thr Gln Leu Asp Ser Ser Thr Ile Val Gln Lys Leu Asn Thr
450 455 460
Lys Ile Phe Gly Ala Ala Phe Ile Asp Thr Ala Thr Gly Glu Leu Gln
465 470 475 480
Met Leu Glu Phe Glu Asp Asp Ser Glu Cys Thr Lys Leu Asp Thr Leu
485 490 495
Met Ser Gln Val Arg Pro Met Glu Val Val Met Glu Arg Asn Asn Leu
500 505 510
Ser Thr Leu Ala Asn Lys Ile Val Lys Phe Asn Ser Ala Pro Asn Ala
515 520 525
Ile Phe Asn Glu Val Lys Ala Gly Glu Glu Phe Tyr Asp Cys Asp Lys
530 535 540
Thr Tyr Ala Glu Ile Ile Ser Ser Glu Tyr Phe Ser Thr Glu Glu Asp
545 550 555 560
Trp Pro Glu Val Leu Lys Ser Tyr Tyr Asp Thr Gly Lys Lys Val Gly
565 570 575
Phe Ser Ala Phe Gly Gly Leu Leu Tyr Tyr Leu Lys Trp Leu Lys Leu

| 580 | 585 | 590 |
|-------------------------------------|---------------------|---------------------|
| Asp Lys Asn Leu Ile Ser Met | Lys Asn Ile Lys Glu | Tyr Asp Phe Val |
| 595 | 600 | 605 |
| Lys Ser Gln His Ser Met Val | Leu Asp Gly Ile Thr | Leu Gln Asn Leu |
| 610 | 615 | 620 |
| Glu Ile Phe Ser Asn Ser Phe | Asp Gly Ser Asp Lys | Gly Thr Leu Phe |
| 625 | 630 | 635 |
| Lys Leu Phe Asn Arg Ala Ile | Thr Pro Met Gly Lys | Arg Met Met Lys |
| 645 | 650 | 655 |
| Lys Trp Leu Met His Pro Leu | Leu Arg Lys Asn Asp | Ile Glu Ser Arg |
| 660 | 665 | 670 |
| Leu Asp Ser Val Asp Ser Leu | Leu Gln Asp Ile Thr | Leu Arg Glu Gln |
| 675 | 680 | 685 |
| Leu Glu Ile Thr Phe Ser Lys | Leu Pro Asp Leu Glu | Arg Met Leu Ala |
| 690 | 695 | 700 |
| Arg Ile His Ser Arg Thr Ile | Lys Val Lys Asp Phe | Glu Lys Val Ile |
| 705 | 710 | 715 |
| Thr Ala Phe Glu Thr Ile Ile | Glu Leu Gln Asp Ser | Leu Lys Asn Asn |
| 725 | 730 | 735 |
| Asp Leu Lys Gly Asp Val Ser Lys | Tyr Ile Ser Ser Phe | Pro Glu Gly |
| 740 | 745 | 750 |
| Leu Val Glu Ala Val Lys Ser Trp | Thr Asn Ala Phe | Glu Arg Gln Lys |
| 755 | 760 | 765 |
| Ala Ile Asn Glu Asn Ile Ile | Val Pro Gln Arg | Gly Phe Asp Ile Glu |
| 770 | 775 | 780 |
| Phe Asp Lys Ser Met Asp Arg Ile | Gln Glu Leu Glu Asp | Glu Leu Met |
| 785 | 790 | 795 |
| Glu Ile Leu Met Thr Tyr Arg Lys | Gln Phe Lys Cys Ser | Asn Ile Gln |
| 805 | 810 | 815 |
| Tyr Lys Asp Ser Gly Lys Glu Ile | Tyr Thr Ile Glu Ile | Pro Ile Ser |
| 820 | 825 | 830 |
| Ala Thr Lys Asn Val Pro Ser Asn | Trp Val Gln Met | Ala Ala Asn Lys |
| 835 | 840 | 845 |
| Thr Tyr Lys Arg Tyr Tyr Ser Asp | Glu Val Arg Ala | Leu Ala Arg Ser |
| 850 | 855 | 860 |
| Met Ala Glu Ala Lys Glu Ile | His Lys Thr Leu Glu | Glu Asp Leu Lys |
| 865 | 870 | 875 |
| Asn Arg Leu Cys Gln Lys Phe | Asp Ala His Tyr Asn | Thr Ile Trp Met |
| 885 | 890 | 895 |
| Pro Thr Ile Gln Ala Ile Ser Asn Ile | Asp Cys Leu Leu | Ala Ile Thr |
| 900 | 905 | 910 |
| Arg Thr Ser Glu Tyr Leu Gly Ala | Pro Ser Cys Arg | Pro Thr Ile Val |
| 915 | 920 | 925 |
| Asp Glu Val Asp Ser Lys Thr Asn | Thr Gln Leu Asn | Gly Phe Leu Lys |
| 930 | 935 | 940 |
| Phe Lys Ser Leu Arg His Pro Cys | Phe Asn Leu Gly | Ala Thr Thr Ala |
| 945 | 950 | 955 |
| Lys Asp Phe Ile Pro Asn Asp Ile | Glu Leu Gly Lys | Glu Gln Pro Arg |
| 965 | 970 | 975 |
| Leu Gly Leu Leu Thr Gly Ala Asn | Ala Ala Gly Lys | Ser Thr Ile Leu |
| 980 | 985 | 990 |
| Arg Met Ala Cys Ile Ala Val Ile | Met Ala Gln Met | Gly Cys Tyr Val |
| 995 | 1000 | 1005 |
| Pro Cys Glu Ser Ala Val Leu | Thr Pro Ile Asp Arg | Ile Met Thr Arg |
| 1010 | 1015 | 1020 |
| Leu Gly Ala Asn Asp Asn Ile | Met Gln Gly Lys | Ser Thr Phe Phe Val |
| 1025 | 1030 | 1035 |
| | | 1040 |

Glu Leu Ala Glu Thr Lys Lys Ile Leu Asp Met Ala Thr Asn Arg Ser
1045 1050 1055
Leu Leu Val Val Asp Glu Leu Gly Arg Gly Gly Ser Ser Asp Gly
1060 1065 1070
Phe Ala Ile Ala Glu Ser Val Leu His His Val Ala Thr His Ile Gln
1075 1080 1085
Ser Leu Gly Phe Phe Ala Thr His Tyr Gly Thr Leu Ala Ser Ser Phe
1090 1095 1100
Lys His His Pro Gln Val Arg Pro Leu Lys Met Ser Ile Leu Val Asp
1105 1110 1115 1120
Glu Ala Thr Arg Asn Val Thr Phe Leu Tyr Lys Met Leu Glu Gly Gln
1125 1130 1135
Ser Glu Gly Ser Phe Gly Met His Val Ala Ser Met Cys Gly Ile Ser
1140 1145 1150
Lys Glu Ile Ile Asp Asn Ala Gln Ile Ala Ala Asp Asn Leu Glu His
1155 1160 1165
Thr Ser Arg Leu Val Lys Glu Arg Asp Leu Ala Ala Asn Asn Leu Asn
1170 1175 1180
Gly Glu Val Val Ser Val Pro Gly Gly Leu Gln Ser Asp Phe Val Arg
1185 1190 1195 1200
Ile Ala Tyr Gly Asp Gly Leu Lys Asn Thr Lys Leu Gly Ser Gly Glu
1205 1210 1215
Gly Val Leu Asn Tyr Asp Trp Asn Ile Lys Arg Asn Val Leu Lys Ser
1220 1225 1230
Leu Phe Ser Ile Ile Asp Asp Leu Gln Ser
1235 1240